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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=8; day=28; hr=14; min=19; sec=6; ms=843; ]

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Application No: 09586704 Version No: 7.0

Input Set:

Output Set:

**Started:** 2009-08-13 18:17:34.096  
**Finished:** 2009-08-13 18:17:38.137  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 41 ms  
**Total Warnings:** 6  
**Total Errors:** 22  
**No. of SeqIDs Defined:** 13  
**Actual SeqID Count:** 13

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)

**Input Set:**

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Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)

# SEQUENCE LISTING

<110> STEINMAN, RALPH A.  
 NUSSENZWEIG, MICHEL C.  
 SWIGGARD, WILLIAM J.  
 JIANG, WANPING

<120> IDENTIFICATION OF DEC, A RECEPTOR WITH  
 C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS  
 ENCODING DEC, AND USES THEREOF

<130> RUJ-001CNRCE2

<140> 09586704

<141> 2000-06-05

<150> 08/381,528

<151> 1995-01-31

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<223> C terminal DEC-205

<400> 1

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	

Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp
			20					25					30

<210> 2

<211> 25

<212> PRT

<213> Mus musculus

<220>

<223> N terminal DEC-205

<400> 2

Ser	Glu	Ser	Ser	Gly	Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Glu	Asn	Thr
1				5					10					15	

Gly	Lys	Cys	Ile	Gln	Pro	Leu	Phe	Asp
			20					25

<210> 3

<211> 1723

<212> PRT

<213> Mus musculus

<220>

<223> Predicted DEC-205

<400> 3

Met	Arg	Thr	Gly	Arg	Val	Thr	Pro	Gly	Leu	Ala	Ala	Gly	Leu	Leu	Leu
1				5					10					15	

Leu	Leu	Leu	Arg	Ser	Phe	Gly	Leu	Val	Glu	Pro	Ser	Glu	Ser	Ser	Gly
			20					25					30		

Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Glu	Asn	Thr	Gly	Lys	Cys	Ile	Gln
		35					40					45			

Pro	Leu	Ser	Asp	Trp	Val	Val	Ala	Gln	Asp	Cys	Ser	Gly	Thr	Asn	Asn
	50					55					60				

Met	Leu	Trp	Lys	Trp	Val	Ser	Gln	His	Arg	Leu	Phe	His	Leu	Glu	Ser
65					70					75				80	

Gln	Lys	Cys	Leu	Gly	Leu	Asp	Ile	Thr	Lys	Ala	Thr	Asp	Asn	Leu	Arg
			85						90					95	

Met	Phe	Ser	Cys	Asp	Ser	Thr	Val	Met	Leu	Trp	Trp	Lys	Cys	Glu	His
			100					105					110		

His	Ser	Leu	Tyr	Thr	Ala	Ala	Gln	Tyr	Arg	Leu	Ala	Leu	Lys	Asp	Gly
		115					120						125		

Tyr	Ala	Val	Ala	Asn	Thr	Asn	Thr	Ser	Asp	Val	Trp	Lys	Lys	Gly	Gly
	130					135					140				

Ser	Glu	Glu	Asn	Leu	Cys	Ala	Gln	Pro	Tyr	His	Glu	Ile	Tyr	Thr	Arg
145				150						155					160

Asp	Gly	Asn	Ser	Tyr	Gly	Arg	Pro	Cys	Glu	Phe	Pro	Phe	Leu	Ile	Gly
				165					170					175	

Glu	Thr	Trp	Tyr	His	Asp	Cys	Ile	His	Asp	Glu	Asp	His	Ser	Gly	Pro
				180				185						190	

Trp	Cys	Ala	Thr	Thr	Leu	Ser	Tyr	Glu	Tyr	Asp	Gln	Lys	Trp	Gly	Ile	195	200	205	
Cys	Leu	Leu	Pro	Glu	Ser	Gly	Cys	Glu	Gly	Asn	Trp	Glu	Lys	Asn	Glu	210	215	220	
Gln	Ile	Gly	Ser	Cys	Tyr	Gln	Phe	Asn	Asn	Gln	Glu	Ile	Leu	Ser	Trp	225	230	235	240
Lys	Glu	Ala	Tyr	Val	Ser	Cys	Gln	Asn	Gln	Gly	Ala	Asp	Leu	Leu	Ser	245	250	255	
Ile	His	Ser	Ala	Ala	Glu	Leu	Ala	Tyr	Ile	Thr	Gly	Lys	Glu	Asp	Ile	260	265	270	
Ala	Arg	Leu	Val	Trp	Leu	Gly	Leu	Asn	Gln	Leu	Tyr	Ser	Ala	Arg	Gly	275	280	285	
Trp	Glu	Trp	Ser	Asp	Phe	Arg	Pro	Leu	Lys	Phe	Leu	Asn	Trp	Asp	Pro	290	295	300	
Gly	Thr	Pro	Val	Ala	Pro	Val	Ile	Gly	Gly	Ser	Ser	Cys	Ala	Arg	Met	305	310	315	320
Asp	Thr	Glu	Ser	Gly	Leu	Trp	Gln	Ser	Val	Ser	Cys	Glu	Ser	Gln	Gln	325	330	335	
Pro	Tyr	Val	Cys	Lys	Lys	Pro	Leu	Asn	Asn	Thr	Leu	Glu	Leu	Pro	Asp	340	345	350	
Val	Trp	Thr	Tyr	Thr	Asp	Thr	His	Cys	His	Val	Gly	Trp	Leu	Pro	Asn	355	360	365	
Asn	Gly	Phe	Cys	Tyr	Leu	Leu	Ala	Asn	Glu	Ser	Ser	Ser	Trp	Asp	Ala	370	375	380	
Ala	His	Leu	Lys	Cys	Lys	Ala	Phe	Gly	Ala	Asp	Leu	Ile	Ser	Met	His	385	390	395	400
Ser	Leu	Ala	Asp	Val	Glu	Val	Val	Val	Thr	Lys	Leu	His	Asn	Gly	Asp	405	410	415	

Val Lys Lys Glu Ile Trp Thr Gly Leu Lys Asn Thr Asn Ser Pro Ala  
420 425 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asn  
435 440 445

Glu Asn Glu Pro Ser Val Pro Phe Asn Lys Thr Pro Asn Cys Val Ser  
450 455 460

Tyr Leu Gly Lys Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Lys Lys  
465 470 475 480

Leu Arg Tyr Val Cys Lys Lys Lys Gly Glu Ile Thr Lys Asp Ala Glu  
485 490 495

Ser Asp Lys Leu Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu  
500 505 510

Thr Cys Tyr Lys Ile Tyr Glu Lys Glu Ala Pro Phe Gly Thr Asn Cys  
515 520 525

Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Phe Leu Asn Tyr Met  
530 535 540

Met Lys Asn Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu  
545 550 555 560

Arg Asp Pro Asp Ser Arg Gly Glu Tyr Ser Trp Ala Val Ala Gln Gly  
565 570 575

Val Lys Gln Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala  
580 585 590

Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Thr Leu Gly Lys  
595 600 605

Trp Glu Val Lys Asn Cys Arg Ser Phe Arg Ala Leu Ser Ile Cys Lys  
610 615 620

Lys Val Ser Glu Pro Gln Glu Pro Glu Glu Ala Ala Pro Lys Pro Asp  
625 630 635 640

Asp Pro Cys Pro Glu Gly Trp His Thr Phe Pro Ser Ser Leu Ser Cys

645	650	655
Tyr Lys Val Phe His Ile Glu Arg Ile Val Arg Lys Arg Asn Trp Glu		
660	665	670
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Pro Ser Phe		
675	680	685
Ser Arg Arg Glu Glu Ile Lys Asp Phe Val His Leu Leu Lys Asp Gln		
690	695	700
Phe Ser Gly Gln Arg Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro		
705	710	715
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Ala		
725	730	735
Val Met Met Glu Pro Glu Phe Gln Gln Asp Phe Asp Ile Arg Asp Cys		
740	745	750
Ala Ala Ile Lys Val Leu Asp Val Pro Trp Arg Arg Val Trp His Leu		
755	760	765
Tyr Glu Asp Lys Asp Tyr Ala Tyr Trp Lys Pro Phe Ala Cys Asp Ala		
770	775	780
Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Ser Thr Pro Gln Met		
785	790	795
Pro Asp Trp Tyr Asn Pro Glu Arg Thr Gly Ile His Gly Pro Pro Val		
805	810	815
Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Pro His Leu Asn		
820	825	830
Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala		
835	840	845
Thr Ile Thr Ser Phe Thr Gly Leu Lys Ala Ile Lys Asn Lys Leu Ala		
850	855	860
Asn Ile Ser Gly Glu Glu Gln Lys Trp Trp Val Lys Thr Ser Glu Asn		
865	870	875
		880



Pro Ile Asp Arg Tyr Phe Leu Gly Ser Arg Arg Arg Leu Trp His His  
885 890 895

Phe Pro Met Thr Phe Gly Asp Glu Cys Leu His Met Ser Ala Lys Thr  
900 905 910

Trp Leu Val Asp Leu Ser Lys Arg Ala Asp Cys Asn Ala Lys Leu Pro  
915 920 925

Phe Ile Cys Glu Arg Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro  
930 935 940

Asp Pro Ala Ala Lys Val Gln Cys Thr Glu Lys Trp Ile Pro Phe Gln  
945 950 955 960

Asn Lys Cys Phe Leu Lys Val Asn Ser Gly Pro Val Thr Phe Ser Gln  
965 970 975

Ala Ser Gly Ile Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu  
980 985 990

Ser Arg Gly Glu Gln Asp Phe Ile Ile Ser Leu Leu Pro Glu Met Glu  
995 1000 1005

Ala Ser Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Arg Ile  
1010 1015 1020

Asn Arg Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His  
1025 1030 1035

Pro Leu Leu Val Gly Arg Arg Leu Ser Ile Pro Thr Asn Phe Phe  
1040 1045 1050

Asp Asp Glu Ser His Phe His Cys Ala Leu Ile Leu Asn Leu Lys  
1055 1060 1065

Lys Ser Pro Leu Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu  
1070 1075 1080

Arg His Ser Leu Ser Leu Cys Gln Lys Tyr Ser Glu Thr Glu Asp  
1085 1090 1095

Gly Gln	Pro Trp Glu Asn Thr	Ser Lys Thr Val Lys	Tyr Leu Asn
1100	1105	1110	
Asn Leu	Tyr Lys Ile Ile Ser	Lys Pro Leu Thr Trp	His Gly Ala
1115	1120	1125	
Leu Lys	Glu Cys Met Lys Glu	Lys Met Arg Leu Val	Ser Ile Thr
1130	1135	1140	
Asp Pro	Tyr Gln Gln Ala Phe	Leu Ala Val Gln Ala	Thr Leu Arg
1145	1150	1155	
Asn Ser	Ser Phe Trp Ile Gly	Leu Ser Ser Gln Asp	Asp Glu Leu
1160	1165	1170	
Asn Phe	Gly Trp Ser Asp Gly	Lys Arg Leu Gln Phe	Ser Asn Trp
1175	1180	1185	
Ala Gly	Ser Asn Glu Gln Leu	Asp Asp Cys Val Ile	Leu Asp Thr
1190	1195	1200	
Asp Gly	Phe Trp Lys Thr Ala	Asp Cys Asp Asp Asn	Gln Pro Gly
1205	1210	1215	
Ala Ile	Cys Tyr Tyr Pro Gly	Asn Glu Thr Glu Glu	Glu Val Arg
1220	1225	1230	
Ala Leu	Asp Thr Ala Lys Cys	Pro Ser Pro Val Gln	Ser Thr Pro
1235	1240	1245	
Trp Ile	Pro Phe Gln Asn Ser	Cys Tyr Asn Phe Met	Ile Thr Asn
1250	1255	1260	
Asn Arg	His Lys Thr Val Thr	Pro Glu Glu Val Gln	Ser Thr Cys
1265	1270	1275	
Glu Lys	Leu His Pro Lys Ala	His Ser Leu Ser Ile	Arg Asn Glu
1280	1285	1290	
Glu Glu	Asn Thr Phe Val Val	Glu Gln Leu Leu Tyr	Phe Asn Tyr
1295	1300	1305	

Ile Ala	Ser Trp Val Met Leu Gly Ile Thr Tyr Glu	Asn Asn Ser
1310	1315	1320
Leu Met	Trp Phe Asp Lys Thr Ala Leu Ser Tyr Thr	His Trp Arg
1325	1330	1335
Thr Gly	Arg Pro Thr Val Lys Asn Gly Lys Phe Leu	Ala Gly Leu
1340	1345	1350
Ser Thr	Asp Gly Phe Trp Asp Ile Gln Ser Phe Asn	Val Ile Glu
1355	1360	1365
Glu Thr	Leu His Phe Tyr Gln His Ser Ile Ser Ala	Cys Lys Ile
1370	1375	1380
Glu Met	Val Asp Tyr Glu Asp Lys His Asn Gly Thr	Leu Pro Gln
1385	1390	1395
Phe Ile	Pro Tyr Lys Asp Gly Val Tyr Ser Val Ile	Gln Lys Lys
1400	1405	1410
Val Thr	Trp Tyr Glu Ala Leu Asn Ala Cys Ser Gln	Ser Gly Gly
1415	1420	1425
Glu Leu	Ala Ser Val His Asn Pro Asn Gly Lys Leu	Phe Leu Glu
1430	1435	1440
Asp Ile	Val Asn Arg Asp Gly Phe Pro Leu Trp Val	Gly Leu Ser
1445	1450	1455
Ser His	Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser	Asp Gly Arg
1460	1465	1470
Ala Phe	Asp Tyr Val Pro Trp Gln Ser Leu Gln Ser	Pro Gly Asp
1475	1480	1485
Cys Val	Val Leu Tyr Pro Lys Gly Ile Trp Arg Arg	Glu Lys Cys
1490	1495	1500
Leu Ser	Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro	Thr Lys Asp
1505	1510	1515

Lys Lys Leu Ile Phe His Val Lys Ser Ser Lys Cys Pro Val Ala  
1520 1525 1530

Lys Arg Asp Gly Pro Gln Trp Val Gln Tyr Gly Gly His Cys Tyr  
1535 1540 1545

Ala Ser Asp Gln Val Leu His Ser Phe Ser Glu Ala Lys Gln Val  
1550 1555 1560

Cys Gln Glu Leu Asp His Ser Ala Thr Val Val Thr Ile Ala Asp  
1565 1570 1575

Glu Asn Glu Asn Lys Phe Val Ser Arg Leu Met Arg Glu Asn Tyr  
1580 1585 1590

Asn Ile Thr Met Arg Val Trp Leu Gly Leu Ser Gln His Ser Leu  
1595 1600 1605

Asp Gln Ser Trp Ser Trp Leu Asp Gly Leu Asp Val Thr Phe Val  
1610 1615 1620

Lys Trp Glu Asn Lys Thr Lys Asp Gly Asp Gly Lys Cys Ser Ile  
1625 1630 1635

Leu Ile Ala Ser Asn Glu Thr Trp Arg Lys Val His Cys Ser Arg  
1640 1645 1650

Gly Tyr Ala Arg Ala Val Cys Lys Ile Pro Leu Ser Pro Asp Tyr  
1655 1660 1665

Thr Gly Ile Ala Ile Leu Phe Ala Val Leu Cys Leu Leu Gly Leu  
1670 1675 1680

Ile Ser Leu Ala Ile Trp Phe Leu Leu Gln Arg Ser His Ile Arg  
1685 1690 1695

Trp Thr Gly Phe Ser Ser Val Arg Tyr Glu His Gly Thr Asn Glu  
1700 1705 1710

Asp Glu Val Met Leu Pro Ser Phe His Asp  
1715 1720

<211> 1462

<212> PRT

<213> Bos Taurus

<220>

<223> PLA2 receptor

<400> 4

Met Pro Leu Leu Ser Leu Ser Leu Leu Leu Leu Leu Gln Val Pro  
1 5 10 15

Ala Gly Ser Ala Glu Thr Ala Ala Trp Ala Val Thr Pro Glu Arg Leu  
20 25 30

Arg Glu Trp Gln Asp Lys Gly Ile Phe Ile Ile Gln Ser Glu Asn Leu  
35 40 45

Glu Lys Cys Ile Gln Ala Ser Lys Ser Thr Leu Thr Leu Glu Asn Cys  
50 55 60

Lys Pro Pro Asn Lys Tyr Met Leu Trp Lys Trp Val Ser Asn His Arg  
65 70 75 80

Leu Phe Asn Ile Gly Gly Ser Gly Cys Leu Gly Leu Asn Val Ser Ser  
85 90 95

Pro Glu Gln Pro Leu Ser Ile Tyr Glu Cys Asp Ser Thr His Val Ser  
100 105 110

Leu Lys Trp His Cys Asn Lys Lys Thr Ile Thr Gly Pro Leu Gln Tyr  
115 120 125

Leu Val Gln Val Lys Gln Asp Asn Thr Leu Val Ala Ser Arg Lys Tyr  
130 135 140

Leu His Lys Trp Val Ser Tyr Met Ser Gly Gly Gly Gly Ile Cys Asp  
145 150 155 160

Tyr Leu His Lys Asp Leu Tyr Thr Ile Lys Gly Asn Ala His Gly Thr  
165 170 175

Pro Cys Met Phe Pro Phe Gln Tyr Asn Gln Gln Trp His His Glu Cys  
180